



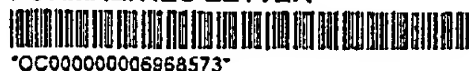
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APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
09/928,048	08/10/2001	Thomas L. Cantor	

CONFIRMATION NO. 7860

FORMALITIES LETTER



OC000000006968573

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Date Mailed: 10/25/2001

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE
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Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

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- To Purchase PatentIn Software, call (703) 306-2600
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BIOTECHNOLOGY
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ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/928,048Source: O/PEDate Processed by STIC: 8/23/2001**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.****PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.****PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)****PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)****TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:****Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/928,048

TIME: 15:01:19

Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I928048.raw

101 <211> LENGTH: 51 ([integer length])
103 <212> TYPE: PRT
105 <213> ORGANISM: human parathyroid hormone peptide fragment
107 <400> SEQUENCE: 5
109 Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp Ala Gly Ser
110 1 5 10 15
112 Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val Glu Ser His
113 20 25 30
115 Glu Lys Ser Leu Gly Glu Ala Asn Lys Ala Asp Val Asn Val Leu
116 35 40 45
E--> 118 Thyr Lys Ala Lys Ser Gln
119 50

VERIFICATION SUMMARY

DATE: 08/23/2001

PATENT APPLICATION: US/09/928,048

TIME: 15:01:20

Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I928048.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
U:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:67 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:67 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:96 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:96 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:118 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:118 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

PATENT APPLICATION: US/09/928,048

TIM 15:01:19

Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I928048.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Cantor, Thomas L.
 6 <120> TITLE OF INVENTION: Methods and Devices for Direct Determination of Cyclase
 nhibiting
 7 Parathyroid Hormone
 9 <140> CURRENT APPLICATION NUMBER: US/09/928,048
 9 <141> CURRENT FILING DATE: 2001-08-10
 0 <130> FILE REFERENCE:
 9 <160> NUMBER OF SEQ ID NOS: 5
 11 <170> SOFTWARE: Microsoft Word 2000 - ASCII format

pp 1-2

ERRORED SEQUENCES

42 <210> SEQ ID NO: 3
 44 <211> LENGTH: 84 (integer length) delete
 46 <212> TYPE: PRT
 48 <213> ORGANISM: human parathyroid hormone peptide fragment
 50 <400> SEQUENCE: 3
 52 Ser Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu
 53 1 5 10 15
 55 Asn Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp
 56 20 25 30
 58 Val His Asn Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp
 59 35 40 45
 61 Ala Gly Ser Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val
 62 50 55 60
 64 Glu Ser His Glu Lys Ser Leu Gly Glu Ala Asn Lys Ala Asp Val
 65 65 70 75
 :--> 67 Asn Val Leu Thyr Lys Ala Lys Ser Gln Invalid
 68 80
 71 <210> SEQ ID NO: 4
 73 <211> LENGTH: 83 (integer length) delete
 75 <212> TYPE: PRT
 77 <213> ORGANISM: human parathyroid hormone peptide fragment
 79 <400> SEQUENCE: 4
 81 Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn
 82 1 5 10 15
 84 Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
 85 20 25 30
 87 His Asn Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp Ala
 88 35 40 45
 90 Gly Ser Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val Glu
 91 50 55 60
 93 Ser His Glu Lys Ser Leu Gly Glu Ala Asn Lys Ala Asp Val Asn
 94 65 70 75
 :--> 96 Val Leu Thyr Lys Ala Lys Ser Gln
 97 80
 99 <210> SEQ ID NO: 5